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<170> PatentIn version 3.3

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Ser Pro Glu Asn Gly Ala Arg Val Val Ala Lys Ala Trp Val Asp Pro
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Gln Phe Arg Ala Leu Leu Lys Asp Gly Thr Ala Ala Cys Ala Gln
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105

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105

110

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195 200 205

Pro Thr Ala Arg Ile Met Pro Met Ala His Gly Asn Ile Pro Ser Ala
210 215 220

Ser Leu Leu Gly Thr His Leu Phe Asp Leu Pro Ser Leu Ala Ala Ser
225 230 235 240

Pro Gly Trp Met Arg Lys Met Glu Ala Ala Asp Ala Pro Ala Ser Glu
245 250 255

Ser Asp Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Glu Arg Ala Pro
260 265 270

Phe His Pro Gln Arg Leu Leu Asp Phe Leu Gln Gln Pro Trp Cys Asn
275 280 285

Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His
290 295 300

Leu Glu Thr Gly Leu Leu Val Gln Ser Gly Lys Arg Phe Gln Trp Asp
305 310 315 320

Tyr Val Gly Arg Trp Trp Asn Phe Ile Glu Pro Ser Gln Trp Pro Arg
325 330 335

Asp Glu Tyr Arg Leu Gln Gly Ile Arg Ala Lys Trp Asp Ser Val Val

340

345

350

Gly Asp Cys Arg Gln Glu Leu Val Phe Ile Gly Gln Gly Leu Asp Thr
355 360 365

Asp Ala Leu Gln Arg Glu Leu Asp His Cys Leu Leu Ser Ala Gln Glu
370 375 380
Ile Ala Ala Gly Pro Leu Ala Trp Gln Ala Leu Pro Gly Ala Thr Ala
385 390 395 400

Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu
405 410 415

Pro Pro Phe Asp Pro Arg
420

<210> 6
<211> 2371
<212> DNA
<213> Pseudomonas putida

<220>
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<222> (1)..(582)
<223> Gen der Kodierregion der alpha-Untereinheit

<220>
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<222> (624)..(1286)
<223> Gen der Kodierregion der beta-Untereinheit

<220>
<221> gene
<222> (1283)..(2371)
<223> Gen des Aktivatorproteins

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Met Thr Ala Thr Ser Thr Pro Gly Glu Arg Ala Arg Ala Leu Phe Ala
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gtg ctc aag cgc aaa gac ctc atc ccc gag ggc tac atc gaa cag ctc 96
Val Leu Lys Arg Lys Asp Leu Ile Pro Glu Gly Tyr Ile Glu Gln Leu
20 25 30

acc cag ctg atg gaa cac ggc tgg agc ccg gaa aac ggc gcg cgc atc 144
Thr Gln Leu Met Glu His Gly Trp Ser Pro Glu Asn Gly Ala Arg Ile
35 40 45

gtc gcc aag gcc tgg gtc gat ccg cag ttt cgc gag ctg ctg ctc aag 192
Val Ala Lys Ala Trp Val Asp Pro Gln Phe Arg Glu Leu Leu Lys
50 55 60

gac ggt acg gcc gcc tgc gcc cag ttc ggc ttc acc ggc cca caa ggc 240
Asp Gly Thr Ala Ala Cys Ala Gln Phe Gly Phe Thr Gly Pro Gln Gly

65	70	75	80	
gaa tac atc gtc gcc ctg gaa gac acc ccg cag ttg aaa aac gtg atc Glu Tyr Ile Val Ala Leu Glu Asp Thr Pro Gln Leu Lys Asn Val Ile 85	90	95		288
gtc tgt agc ctg tgc tcc tgc acg aac tgg ccg gtg ctg ggc ctg cca Val Cys Ser Leu Cys Ser Cys Thr Asn Trp Pro Val Leu Gly Leu Pro 100	105	110		336
cct gag tgg tac aag ggc ttc gag ttc cgt gcg cgg ttg gtc cgg gag Pro Glu Trp Tyr Lys Gly Phe Glu Phe Arg Ala Arg Leu Val Arg Glu 115	120	125		384
ggg cgc acg gta ttg cgc gag ctg ggc acc gag ttg ccc ggc gac atg Gly Arg Thr Val Leu Arg Glu Leu Gly Thr Glu Leu Pro Gly Asp Met 130	135	140		432
gtg gtc aag gtc tgg gac acc agc gct gaa agc cgc tac ctg gtg ctg Val Val Lys Val Trp Asp Thr Ser Ala Glu Ser Arg Tyr Leu Val Leu 145	150	155	160	480
ccg caa cga cca gcg ggc tca gag cat atg agc gaa gag cag ttg cgg Pro Gln Arg Pro Ala Gly Ser Glu His Met Ser Glu Glu Gln Leu Arg 165	170	175		528
caa ctg gtc acc aag gac gtg ctg atc ggc gtc gcc ctg ccc cgc gtt Gln Leu Val Thr Lys Asp Val Leu Ile Gly Val Ala Leu Pro Arg Val 180	185	190		576
ggc tga gcaaggccgc ccaacccat tcaacttccg gagtgttcaa t atg gat ggc Gly			Met Asp Gly 195	632
ttt cac gat ctc ggc ggt ttc cag ggc ttt ggc aaa gtg ccc cac cgc Phe His Asp Leu Gly Gly Phe Gln Gly Phe Gly Lys Val Pro His Arg 200	205	210		680
atc aac agc ctg agc tac aag cag gtg ttc aag cag gac tgg gaa cac Ile Asn Ser Leu Ser Tyr Lys Gln Val Phe Lys Gln Asp Trp Glu His 215	220	225		728
ctg gcc tac agc ctg atg ttc atc ggc gtc gac cac ctg aac aag ttc Leu Ala Tyr Ser Leu Met Phe Ile Gly Val Asp His Leu Asn Lys Phe 230	235	240		776
agc gtc gac gaa ata cgt cat gcc gtc gaa cgc att gac gtg cgc cag Ser Val Asp Glu Ile Arg His Ala Val Glu Arg Ile Asp Val Arg Gln 245	250	255	260	824
cac gtc ggc acc gaa tac tac gaa cgt tat gtg atc gcc act gcc acg His Val Gly Thr Glu Tyr Tyr Glu Arg Tyr Val Ile Ala Thr Ala Thr 265	270	275		872
ctg ctg gtc gaa aca ggc gtc atc acc cag gcc gaa ctg gat gaa gca Leu Leu Val Glu Thr Gly Val Ile Thr Gln Ala Glu Leu Asp Glu Ala 280	285	290		920
ctc ggc tcg cac ttc aag ctg gcc aac ccc gcc cat gcg caa ggg cgt Leu Gly Ser His Phe Lys Leu Ala Asn Pro Ala His Ala Gln Gly Arg 295	300	305		968

gct gca att atc ggg cga gcg cct ttt gaa gtg ggc gat cgg gtc atc Ala Ala Ile Ile Gly Arg Ala Pro Phe Glu Val Gly Asp Arg Val Ile 310 315 320	1016
gta cgc gat gaa tac gtg gcc ggg cat gtg cgc atg cct gca tac gtg Val Arg Asp Glu Tyr Val Ala Gly His Val Arg Met Pro Ala Tyr Val 325 330 335 340	1064
cgc ggc aag caa ggc gta gtg ctg cac cgg acc act gaa cag tgg ccg Arg Gly Lys Gln Gly Val Val Leu His Arg Thr Thr Glu Gln Trp Pro 345 350 355	1112
ttt ccg gac gcg att ggc cat ggc gac cag agc gct gcg cat caa ccg Phe Pro Asp Ala Ile Gly His Gly Asp Gln Ser Ala Ala His Gln Pro 360 365 370	1160
acc tac cat gtc gag ttc cgc gtg cgg gac ctg tgg ggc gat gcc gca Thr Tyr His Val Glu Phe Arg Val Arg Asp Leu Trp Gly Asp Ala Ala 375 380 385	1208
gac gac ggc ctg gtg gta gac ctg ttc gaa agc tat ctg gac agg Asp Asp Gly Leu Val Val Asp Leu Phe Glu Ser Tyr Leu Asp Arg 390 395 400	1256
gtc gaa agc ccg cga gtg gtg cgc gca tga gtgcggcgc ccaggcaggc Val Glu Ser Pro Arg Val Val Arg Ala 405 410	1306
cggctgccgg tgacggtcct ttcaggcttc ctcggcgca gcaagaccac cctgctcaac	1366
cacatcctgc gcaaccgcca gggcctgaag gtggcggta tcgtcaatga catgagcgag	1426
gtcaacatcg atgcccggca ggtccagcgc gacgttgcgc tgtatcgtgg ccaggatgaa	1486
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acccagctgt tcgatttgcc cagccttgcc gcagcgcccg gctggatgaa acagatggac	2026
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gcmcgcgcgg cgttccatcc gcaacgcttg cttgatttc tcgccccggcc ctggcgcgac	2146
ggccgtcttc tgcgcagcaa aggttatttc tggcttgcca gccgccaccg cgaaatcgcc	2206

ttgctggta c acagcggcca gcagttcaa tggactatg ttggccattg gtggaaactc	2266
atcgacacgt cacagtggcc acaggacaag tatcgcttgc agggcatcat ggccaagtgg	2326
gacagcatcg tcggcgactg ccgacaggag ctgaaaagct tatga	2371
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30	
Thr Gln Leu Met Glu His Gly Trp Ser Pro Glu Asn Gly Ala Arg Ile	
35	40
45	
Val Ala Lys Ala Trp Val Asp Pro Gln Phe Arg Glu Leu Leu Leu Lys	
50	55
60	
Asp Gly Thr Ala Ala Cys Ala Gln Phe Gly Phe Thr Gly Pro Gln Gly	
65	70
75	80
Glu Tyr Ile Val Ala Leu Glu Asp Thr Pro Gln Leu Lys Asn Val Ile	
85	90
95	
Val Cys Ser Leu Cys Ser Cys Thr Asn Trp Pro Val Leu Gly Leu Pro	
100	105
110	
Pro Glu Trp Tyr Lys Gly Phe Glu Phe Arg Ala Arg Leu Val Arg Glu	
115	120
125	
Gly Arg Thr Val Leu Arg Glu Leu Gly Thr Glu Leu Pro Gly Asp Met	
130	135
140	
Val Val Lys Val Trp Asp Thr Ser Ala Glu Ser Arg Tyr Leu Val Leu	
145	150
155	160
Pro Gln Arg Pro Ala Gly Ser Glu His Met Ser Glu Glu Gln Leu Arg	
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Gln Leu Val Thr Lys Asp Val Leu Ile Gly Val Ala Leu Pro Arg Val	
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Gly

<210> 8
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<212> PRT
<213> Pseudomonas putida

<400> 8

Met Asp Gly Phe His Asp Leu Gly Gly Phe Gln Gly Phe Gly Lys Val
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Pro His Arg Ile Asn Ser Leu Ser Tyr Lys Gln Val Phe Lys Gln Asp
20 25 30

Trp Glu His Leu Ala Tyr Ser Leu Met Phe Ile Gly Val Asp His Leu
35 40 45

Asn Lys Phe Ser Val Asp Glu Ile Arg His Ala Val Glu Arg Ile Asp
50 55 60

Val Arg Gln His Val Gly Thr Glu Tyr Tyr Glu Arg Tyr Val Ile Ala
65 70 75 80

Thr Ala Thr Leu Leu Val Glu Thr Gly Val Ile Thr Gln Ala Glu Leu
85 90 95

Asp Glu Ala Leu Gly Ser His Phe Lys Leu Ala Asn Pro Ala His Ala
100 105 110

Gln Gly Arg Ala Ala Ile Ile Gly Arg Ala Pro Phe Glu Val Gly Asp
115 120 125

Arg Val Ile Val Arg Asp Glu Tyr Val Ala Gly His Val Arg Met Pro
130 135 140

Ala Tyr Val Arg Gly Lys Gln Gly Val Val Leu His Arg Thr Thr Glu
145 150 155 160

Gln Trp Pro Phe Pro Asp Ala Ile Gly His Gly Asp Gln Ser Ala Ala
165 170 175

His Gln Pro Thr Tyr His Val Glu Phe Arg Val Arg Asp Leu Trp Gly
180 185 190

Asp Ala Ala Asp Asp Gly Leu Val Val Val Asp Leu Phe Glu Ser Tyr
 195 200 205

Leu Asp Arg Val Glu Ser Pro Arg Val Val Arg Ala
 210 215 220

<210> 9
 <211> 1089
 <212> DNA
 <213> Pseudomonas putida

<220>
 <221> CDS
 <222> (1)..(1089)
 <223> Gen der Kodierregion des Aktivatorproteins

<400> 9

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Met	Ser	Ala	Gly	Ala	Gln	Ala	Gly	Arg	Leu	Pro	Val	Thr	Val	Leu	Ser	
1	5	10	15													

ggc ttc ctc ggc gca ggc aag acc acc ctg ctc aac cac atc ctg cgc
 Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg
 20 25 30

aac cgc cag ggc ctg aag gtg gcg gtt atc gtc aat gac atg agc gag
 Asn Arg Gln Gly Leu Lys Val Ala Val Ile Val Asn Asp Met Ser Glu
 35 40 45

gtc aac atc gat gcc gcc cag gtc cag cgc gac gtt gcg ctg tat cgt
 Val Asn Ile Asp Ala Ala Gln Val Gln Arg Asp Val Ala Leu Tyr Arg
 50 55 60

ggc cag gat gaa ttg ata gag atg agc aac ggc tgt atc tgc tgc acc
 Gly Gln Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr
 65 70 75 80

ctg cgc gcc gac ctg ctt gag cag atc agc gcg ctg gcg cgc cag cag
 Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Ala Leu Ala Arg Gln Gln
 85 90 95

cgt ttc gat tac ctg ttg atc gag tcc acc ggg att tcc gag ccg atg
 Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met
 100 105 110

cca gtc gcc gag acc ttt gcc ttt ctc gac gcc aac ggt ttc agc ctc
 Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asn Gly Phe Ser Leu
 115 120 125

agc gaa ctg gcg cgg ctg gat acg ctg gtg acg gtg gtc gat gcc agc
 Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Ala Ser
 130 135 140

cag ttc atg gcc atg ctc gac tct ccc gaa acc gtc gcg cgg gcc gac
 Gln Phe Met Ala Met Leu Asp Ser Pro Glu Thr Val Ala Arg Ala Asp
 145 150 155 160

gtc acc acg gat gac agc agg cgc ccg ctg gcc gat ctg ctg atc gag

Val	Thr	Thr	Asp	Asp	Ser	Arg	Arg	Pro	Leu	Ala	Asp	Leu	Leu	Ile	Glu	
165									170					175		
cag	gtc	gag	tat	gcc	aat	gtg	att	ctg	gtc	aac	aaa	cgc	gac	ctg	gtc	576
Gln	Val	Glu	Tyr	Ala	Asn	Val	Ile	Leu	Val	Asn	Lys	Arg	Asp	Leu	Val	
180								185					190			
gac	gag	gcg	cag	tac	cag	gcc	ctg	cag	gca	gtt	ctc	gcc	ggg	ctc	aat	624
Asp	Glu	Ala	Gln	Tyr	Gln	Ala	Leu	Gln	Ala	Val	Leu	Ala	Gly	Leu	Asn	
195							200					205				
cca	ggc	gca	cag	atc	ctg	ccg	atg	gtg	gcc	ggc	aac	gtc	gcc	ctg	tcg	672
Pro	Gly	Ala	Gln	Ile	Leu	Pro	Met	Val	Ala	Gly	Asn	Val	Ala	Leu	Ser	
210						215					220					
agc	gtc	ctt	ggt	acc	cag	ctg	ttc	gat	ttg	ccc	agc	ctt	gcc	gca	gcg	720
Ser	Val	Leu	Gly	Thr	Gln	Leu	Phe	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Ala	
225					230				235				240			
ccc	ggc	tgg	atg	aaa	cag	atg	gac	gcg	cac	gac	acc	ccg	gcc	ggc	gag	768
Pro	Gly	Trp	Met	Lys	Gln	Met	Asp	Ala	His	Asp	Thr	Pro	Ala	Gly	Glu	
245						250					255					
tcg	cag	acc	tat	ggc	gtg	acg	tca	tgg	gtg	tac	cga	gcg	cgc	gcc	ccg	816
Ser	Gln	Thr	Tyr	Gly	Val	Thr	Ser	Trp	Val	Tyr	Arg	Ala	Arg	Ala	Pro	
260						265					270					
ttc	cat	ccg	caa	cgc	ttg	ctt	gat	ttt	ctc	gcc	cg	ccc	tgg	cg	gac	864
Phe	His	Pro	Gln	Arg	Leu	Leu	Asp	Phe	Leu	Ala	Arg	Pro	Trp	Arg	Asp	
275						280					285					
ggc	cgt	ctt	ctg	cgc	agc	aaa	ggt	tat	ttc	tgg	ctt	gcc	agc	cg	cac	912
Gly	Arg	Leu	Leu	Arg	Ser	Lys	Gly	Tyr	Phe	Trp	Leu	Ala	Ser	Arg	His	
290						295					300					
cgc	gaa	atc	ggc	ttg	ctg	gta	cac	agc	ggc	cag	cag	ttt	caa	tgg	gac	960
Arg	Glu	Ile	Gly	Leu	Leu	Val	His	Ser	Gly	Gln	Gln	Phe	Gln	Trp	Asp	
305						310					315			320		
tat	gtt	ggc	cat	tgg	tgg	aac	ttc	atc	gac	acg	tca	cag	tgg	cca	cag	1008
Tyr	Val	Gly	His	Trp	Trp	Asn	Phe	Ile	Asp	Thr	Ser	Gln	Trp	Pro	Gln	
325						330					335					
gac	aag	tat	cgc	ttg	cag	ggc	atc	atg	gcc	aag	tgg	gac	agc	atc	gtc	1056
Asp	Lys	Tyr	Arg	Leu	Gln	Gly	Ile	Met	Ala	Lys	Trp	Asp	Ser	Ile	Val	
340						345					350					
ggc	gac	tgc	cga	cag	gag	ctg	aaa	agc	tta	tga						1089
Gly	Asp	Cys	Arg	Gln	Glu	Leu	Lys	Ser	Leu							
355						360										
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20 25 30

Asn Arg Gln Gly Leu Lys Val Ala Val Ile Val Asn Asp Met Ser Glu
35 40 45

Val Asn Ile Asp Ala Ala Gln Val Gln Arg Asp Val Ala Leu Tyr Arg
50 55 60

Gly Gln Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr
65 70 75 80

Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Ala Leu Ala Arg Gln Gln
85 90 95

Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met
100 105 110

Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asn Gly Phe Ser Leu
115 120 125

Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Ala Ser
130 135 140

Gln Phe Met Ala Met Leu Asp Ser Pro Glu Thr Val Ala Arg Ala Asp
145 150 155 160

Val Thr Thr Asp Asp Ser Arg Arg Pro Leu Ala Asp Leu Leu Ile Glu
165 170 175

Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Arg Asp Leu Val
180 185 190

Asp Glu Ala Gln Tyr Gln Ala Leu Gln Ala Val Leu Ala Gly Leu Asn
195 200 205

Pro Gly Ala Gln Ile Leu Pro Met Val Ala Gly Asn Val Ala Leu Ser
210 215 220

Ser Val Leu Gly Thr Gln Leu Phe Asp Leu Pro Ser Leu Ala Ala Ala
225 230 235 240

Pro Gly Trp Met Lys Gln Met Asp Ala His Asp Thr Pro Ala Gly Glu
245 250 255

Ser Gln Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Ala Arg Ala Pro

260

265

270

Phe His Pro Gln Arg Leu Leu Asp Phe Leu Ala Arg Pro Trp Arg Asp
275 280 285

Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His
290 295 300

Arg Glu Ile Gly Leu Leu Val His Ser Gly Gln Gln Phe Gln Trp Asp
305 310 315 320

Tyr Val Gly His Trp Trp Asn Phe Ile Asp Thr Ser Gln Trp Pro Gln
325 330 335
Asp Lys Tyr Arg Leu Gln Gly Ile Met Ala Lys Trp Asp Ser Ile Val
340 345 350

Gly Asp Cys Arg Gln Glu Leu Lys Ser Leu
355 360

<210> 11

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<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 1F

<400> 11

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30

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 1R

<400> 12

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<210> 13

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 2F

<400> 13

atgacggcaa cttcaacccc tggtg

25

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

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<223> Primer 2R

<400> 14
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20